

What is Claimed is:

1. A purified and isolated nucleic acid encoding GLUTx.
2. The nucleic acid of Claim 1 that is derived from a human, a mouse or a rat.
3. The nucleic acid of Claim 2 that is derived from a human.
4. The nucleic acid of Claim 2 that is derived from mouse.
5. The nucleic acid of Claim 2 that is derived from a rat.
6. The nucleic acid of Claim 3 which encodes the amino acid sequence for GLUTx shown in Figure 10.
7. The nucleic acid of Claim 6, having the nucleotide sequence for GLUTx as shown in Figure 9.
8. The nucleic acid of Claim 4 which encodes the amino acid sequence for GLUTx shown in Figure 12.
9. The nucleic acid of Claim 8, having the nucleotide sequence for GLUTx as shown in Figure 11.
10. The nucleic acid of Claim 5 which encodes the amino acid sequence for GLUTx shown in Figure 14.
11. The nucleic acid of Claim 10, having the nucleotide sequence for GLUTx as shown in Figure 13.
12. A vector comprising a nucleic acid encoding GLUTx.
13. A host cell transformed by the vector of Claim 12.
14. A method for producing recombinant GLUTx comprising growing a host cell transformed with the vector of Claim 12 and isolating the recombinant GLUTx from said culture.
15. The method of Claim 14, wherein said host cell is a prokaryotic cell.
16. The method of Claim 14, wherein said host cell is a eukaryotic cell.
17. A purified GLUTx protein or an analogue thereof.
18. The purified GLUTx protein of Claim 17 which is recombinantly produced.
19. A nucleic acid probe which hybridizes to nucleic acid encoding GLUTx.

20. The nucleic acid of Claim 1 having one or more mutations.
21. The nucleic acid of Claim 20, wherein the mutations are selected from the group consisting of a point, insertion, rearrangement or deletion mutation.
22. An agent that binds to the protein of Claim 17.
23. The agent of Claim 22, which is an antibody, a peptide, a protein, a nucleic acid, a drug, or antisense nucleic acid.
24. The agent of Claim 23 which is an agonist of GLUTx.
25. An isolated nucleic acid comprising a nucleotide sequence which is at least 80% homologous with the nucleic acid sequence of Claim 1.
26. An isolated nucleic acid comprising a nucleotide sequence which is at least 85% homologous with the nucleic acid sequence of Claim 1.
27. An isolated nucleic acid comprising a nucleotide sequence which is at least 90% homologous with the nucleic acid sequence of Claim 1.
28. An isolated nucleic acid comprising a nucleotide sequence which is at least 95% homologous with the nucleic acid sequence of Claim 1.
29. An isolated nucleic acid comprising a nucleotide sequence which is at least 98% homologous with the nucleic acid sequence of Claim 1.
30. A non-human, transgenic animal model comprising a nucleic acid encoding GLUTx incorporated into some of the somatic cells of said animal.
31. The animal model of Claim 30, wherein said nucleic acid encodes a functional GLUTx protein.
32. The animal model of Claim 31, wherein said nucleic acid has one or more mutations.
33. An agent that binds to the nucleic acid of Claim 1.
34. An agent that enhances the expression of the nucleic acid of Claim 1.
35. The agent of Claim 34, which is a transcription factor, an activator, or a repressor.
36. A method for screening for an agent that binds to the nucleic acid of Claim 1 comprising contacting the nucleic acid with an agent of interest and assessing the ability of the agent to bind to the nucleic acid.

37. A method for screening for an agent that enhances the expression of the nucleic acid of Claim 1 comprising contacting a cell transformed with a vector comprising the nucleic acid, and assessing the effect of the agent on expression of the nucleic acid.

38. A method for screening for an agent that binds to the protein of Claim 17 comprising contacting the protein with an agent of interest and assessing the ability of the agent to bind to the protein.

39. A method of treating type-II diabetes comprising administering to a subject a nucleic acid molecule comprising a nucleotide sequence encoding the amino acid sequence of Figure 10, such that said nucleic acid sequence is expressed in target cells of the patient thereby alleviating the type-II diabetes.

40. The method of Claim 39, wherein the nucleic acid is transfected into target cells by infection with a replication defective virus or by transfection with a liposome comprising said nucleic acid.

41. The method of Claim 40, wherein the target cells are skeletal muscle cells.

42. The method of Claim 41, wherein the nucleic acid molecule comprises the nucleotide sequence of Figure 9.

43. A method of treating type-II diabetes in a subject comprising administering to a subject the agent of Claim 24 or 34 with a physiologically acceptable carrier in an amount effective to treat type-II diabetes in the subject.

add C1

SEQUENCE LISTING

<110> Charron, Maureen
Katz, Ellen

<120> NOVEL GLUCOSE TRANSPORTER/SENSOR PROTEIN AND USES THEREOF

<130> 96700/613

<140> US 09/516,493

<141> 2000-03-01

<150> US 09/356,602

<151> 1999-07-19

<160> 12

<170> PatentIn version 3.0

<210> 1

<211> 98

<212> PRT

<213> mouse

<400> 1

Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Ile Gly Pro Gly
1 5 10 15

Pro Ile Pro Trp Phe Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro
20 25 30

Ala Ala Met Ala Val Arg Gly Phe Ser Asn Trp Thr Cys Asn Phe Ile
35 40 45

Val Gly Met Gly Phe Gln Tyr Val Ala Asp Arg Met Gly Pro Tyr Val
50 55 60

Phe Leu Leu Phe Ala Val Leu Leu Leu Gly Phe Phe Ile Phe Thr Phe
65 70 75 80

Leu Lys Val Pro Glu Thr Arg Gly Arg Thr Phe Asp Gln Ile Ser Ala
85 90 95

Ala Phe

<210> 2

<211> 100

<212> PRT

<213> mouse

<400> 2

Val Gly Ser Met Cys Leu Phe Ile Ala Gly Phe Arg Val Gly Trp Gly
1 5 10 15

Pro Ile Pro Trp Leu Leu Met Ser Glu Ile Phe Pro Leu His Ile Lys
 20 25 30
 Gly Val Ala Thr Gly Val Cys Val Leu Thr Asn Trp Phe Met Ala Phe
 35 40 45
 Leu Val Thr Lys Glu Phe Asn Ser Ile Met Glu Ile Leu Arg Pro Tyr
 50 55 60
 Gly Ala Phe Trp Leu Thr Ala Ala Phe Cys Ile Leu Ser Val Leu Phe
 65 70 75 80
 Thr Leu Thr Phe Val Pro Glu Thr Lys Gly Arg Thr Leu Glu Gln Ile
 85 90 95
 Thr Ala His Phe
 100

<210> 3

<211> 50

<212> PRT

<213> Saccharomyces

<400> 3

Ile Ala Phe Ile Cys Leu Phe Ile Ala Ala Phe Ser Ala Thr Trp Gly
 1 5 10 15
 Gly Val Val Trp Val Val Ser Ala Glu Leu Tyr Pro Leu Gly Val Arg
 20 25 30
 Ser Lys Cys Thr Ala Ile Cys Ala Ala Ala Asn Trp Leu Val Asn Phe
 35 40 45
 Thr Cys
 50

<210> 4

<211> 50

<212> PRT

<213> Saccharomyces

<400> 4

Ile Ala Phe Ile Cys Leu Phe Ile Ala Ala Phe Ser Ala Thr Trp Gly
 1 5 10 15
 Gly Val Val Trp Val Ile Ser Ala Glu Leu Tyr Pro Leu Gly Val Arg
 20 25 30
 Ser Lys Cys Thr Ala Ile Cys Ala Ala Ala Asn Trp Leu Val Asn Phe
 35 40 45
 Ile Cys
 50

<210> 5

<211> 50

<212> PRT

<213> Saccharomyces

<400> 5

Val Gly Ser Met Cys Leu Phe Ile Ala Gly Phe Arg Val Gly Trp Gly
1 5 10 15

Pro Ile Pro Trp Leu Leu Met Ser Glu Ile Phe Pro Leu His Ile Lys
20 25 30

Gly Val Ala Thr Gly Val Cys Val Leu Thr Asn Trp Phe Met Ala Phe
35 40 45

Leu Val
50

<210> 6

<211> 1813

<212> DNA

<213> homo sapiens

<220>

<221> Unsure

<222> (1697)..(1697)

<223> 'n' may be any one of a, t, c, or g

<400> 6

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| aacttgccgc | cgccgcgtct | tctcgcgcgc | cttcgcgcgt | gccctggggc | cactcagctt | 60 |
| cggcttcgcg | ctcggctaca | gctccccggc | catccctagc | ctgcagcgcg | ccgcgcccc | 120 |
| ggccccgcgc | ctggacgacg | ccgcgcctc | ctggttcggg | gctgtcgtga | ccctgggtgc | 180 |
| cgcggcgggg | ggagtgcctg | gcggtggct | ggtggaccgc | gccgggcgca | agctgagcct | 240 |
| cttgcctgtc | tccgtgccct | tcttgccgg | ctttgccgtc | atcaccgcgg | cccaggacgt | 300 |
| gtggatgctg | ctggggggcc | gcctcctcac | cggcctggcc | tgcggtgttg | cctccctagt | 360 |
| ggccccggtc | tacatctccg | aaatgccta | cccagcagtc | cgggggttgc | tcggtcctg | 420 |
| tgtgcagcta | atggtcgtcg | tccgcatact | cctggcctac | ctggcaggct | gggtgctgga | 480 |
| gtggcgctgg | ctggctgtgc | tgggctgcgt | gccccctcc | ctcatgctgc | ttctcatgtg | 540 |
| cttcatgccc | gagacccgcg | gcttctgtct | gactcagcac | aggcgccagg | aggccatcgc | 600 |
| cctgcggttc | ctgtggggct | ccgagcaggg | ctgggaagac | cccccatcg | gggtgagca | 660 |

gagctttcac ctggccctgc tgcggcagcc cggcatctac aagcccttca tcatcggtgt 720
ctccctgatg gccttcacagc agctgtcggg ggtcaacgcc gtcattgtct atgcagagac 780
catctttgaa gaggccaagt tcaaggacag cagcctggcc tcggtcgtcg tgggtgtcat 840
ccagggtgctg ttcacagctg tggcggtctt catcatggac agagcagggc ggaggctgct 900
cctggtcttg tcagggtgtg tcatggtgtt cagcacgagt gccttcggcg cctacttcaa 960
gctgacccag ggtggccctg gcaactcctc gcacgtggcc atctcggcgc ctgtctctgc 1020
acagcctgtt gatgccagcg tggggctggc ctggctggcc gtgggcagca tgtgcctctt 1080
catcgccggc tttgcgggtg gctggggggc catcccttg ctctcatgt cagagatctt 1140
ccctctgcat gtcaagggcg tggcgacagg catctgcgtc ctcaccaact ggctcatggc 1200
ctttctcgtg accaaggagt tcagcagcct catggaggtc ctcaggccct atggagcctt 1260
ctggcttgcc tccgctttct gcattctcag tgtccttttc actttgttct gtgtccctga 1320
aactaaagga aagactcttg aacaaatcac agccatttt gaggggcat gacagccact 1380
cactagggga tggagcaagc ctgtgactcc aagctggggc caagcccaga gcccctgcct 1440
gccccagggg agccagaatc cagccccttg gagccttggc ctgcagggc cctccttctt 1500
gtcatgctcc ctccagccca tgaccggggg ctaggaggct cactgcctcc tgttccagct 1560
cctgctgctg ctctgaggac tcaggaacac cttcagactt tgcagacctg cggtcagccc 1620
tccatgcgca agactaaagc agcgaagag gaggtggggc tctaggatct ttgtcttctg 1680
gctggagggtg cttttgnagg ttgggtgctg ggcattcggc cgctcctctc acgcggtgc 1740
cttatcgga aggaatttg tttgccaaat aaagacgtga cacagaaaat caaaaaaaaa 1800
aaaaaaaaat tcc 1813

<210> 7

<211> 453

<212> PRT

<213> homo sapiens

<400> 7

Arg Arg Val Phe Leu Ala Ala Phe Ala Ala Ala Leu Gly Pro Leu Ser
1 5 10 15
Phe Gly Phe Ala Leu Gly Tyr Ser Ser Pro Ala Ile Pro Ser Leu Gln
20 25 30
Arg Ala Ala Pro Pro Ala Pro Arg Leu Asp Asp Ala Ala Ala Ser Trp
35 40 45
Phe Gly Ala Val Val Thr Leu Gly Ala Ala Ala Gly Gly Val Leu Gly
50 55 60
Gly Trp Leu Val Asp Arg Ala Gly Arg Lys Leu Ser Leu Leu Leu Cys
65 70 75 80

Ser Val Pro Phe Val Ala Gly Phe Ala Val Ile Thr Ala Ala Gln Asp
 85 90 95
 Val Trp Met Leu Leu Gly Gly Arg Leu Leu Thr Gly Leu Ala Cys Gly
 100 105 110
 Val Ala Ser Leu Val Ala Pro Val Tyr Ile Ser Glu Ile Ala Tyr Pro
 115 120 125
 Ala Val Arg Gly Leu Leu Gly Ser Cys Val Gln Leu Met Val Val Val
 130 135 140
 Gly Ile Leu Leu Ala Tyr Leu Ala Gly Trp Val Leu Glu Trp Arg Trp
 145 150 155 160
 Leu Ala Val Leu Gly Cys Val Pro Pro Ser Leu Met Leu Leu Leu Met
 165 170 175
 Cys Phe Met Pro Glu Thr Pro Arg Phe Leu Leu Thr Gln His Arg Arg
 180 185 190
 Gln Glu Ala Ile Ala Leu Arg Phe Leu Trp Gly Ser Glu Gln Gly Trp
 195 200 205
 Glu Asp Pro Pro Ile Gly Ala Glu Gln Ser Phe His Leu Ala Leu Leu
 210 215 220
 Arg Gln Pro Gly Ile Tyr Lys Pro Phe Ile Ile Gly Val Ser Leu Met
 225 230 235 240
 Ala Phe Gln Gln Leu Ser Gly Val Asn Ala Val Met Phe Tyr Ala Glu
 245 250 255
 Thr Ile Phe Glu Glu Ala Lys Phe Lys Asp Ser Ser Leu Ala Ser Val
 260 265 270
 Val Val Gly Val Ile Gln Val Leu Phe Thr Ala Val Ala Ala Leu Ile
 275 280 285
 Met Asp Arg Ala Gly Arg Arg Leu Leu Leu Val Leu Ser Gly Val Val
 290 295 300
 Met Val Phe Ser Thr Ser Ala Phe Gly Ala Tyr Phe Lys Leu Thr Gln
 305 310 315 320
 Gly Gly Pro Gly Asn Ser Ser His Val Ala Ile Ser Ala Pro Val Ser
 325 330 335
 Ala Gln Pro Val Asp Ala Ser Val Gly Leu Ala Trp Leu Ala Val Gly
 340 345 350
 Ser Met Cys Leu Phe Ile Ala Gly Phe Ala Val Gly Trp Gly Pro Ile
 355 360 365
 Pro Trp Leu Leu Met Ser Glu Ile Phe Pro Leu His Val Lys Gly Val
 370 375 380
 Ala Thr Gly Ile Cys Val Leu Thr Asn Trp Leu Met Ala Phe Leu Val
 385 390 395 400
 Thr Lys Glu Phe Ser Ser Leu Met Glu Val Leu Arg Pro Tyr Gly Ala
 405 410 415

Phe Trp Leu Ala Ser Ala Phe Cys Ile Phe Ser Val Leu Phe Thr Leu
420 425 430

Phe Cys Val Pro Glu Thr Lys Gly Lys Thr Leu Glu Gln Ile Thr Ala
435 440 445

His Phe Glu Gly Arg
450

<210> 8

<211> 53

<212> PRT

<213> homo sapiens

<220>

<221> varsplic

<222> (1)..(53)

<223> possible alternate carboxy terminus of predicted
amino acid sequence of human GLUTx protein

<400> 8

Gln Pro Leu Thr Arg Gly Trp Ser Lys Pro Val Thr Pro Ser Trp Ala
1 5 10 15

Gln Ala Gln Ser Pro Cys Leu Pro Gln Gly Ser Gln Asn Pro Ala Pro
20 25 30

Trp Ser Leu Gly Leu Gln Gly Pro Ser Phe Leu Ser Cys Ser Leu Gln
35 40 45

Pro Met Thr Arg Gly
50

<210> 9

<211> 1037

<212> DNA

<213> rat

<220>

<221> unsure

<222> (606)..(609)

<223> 'n' may be any one of a, t, c, or g

<400> 9

tggcggccgc tctagaacta gtggatcccc cgggctgcag gaattcggca cgagctggtg 60

cccatctccg cagagcctgc tgatgttcac ctggggctgg cctggctggc tgtaggcagc 120

atgtgcctct tcatcgctgg ttttgcagta ggctggggac ccatccctg gctcctcatg 180

tcagagatct tccctctgca catcaagggg gtggctaccg gcgtctgtgt cctcaccaac 240
 tggttcatgg cctttctggt gaccaaagag tttaacagca tcatggagat cctcagaccc 300
 tacggcgctt tctggctcac cgtgccttc tgtatcctca gcgtcctttt cacgctcacc 360
 tttgtccctg agactaaagg caggactctg gaacaaatca cagcccattt gagggacggg 420
 gacggacccc tttctgtgac tggcagccct gagctgagct ggcttcgggt ttcaaaagga 480
 gtggagtggc ctcagtgacc acagtttgag ccagggggcc cctgactcc tcagatttcc 540
 gggccagctt tgtccagatc tcaaccacaga ttccacacca tgagcttcac cagattctga 600
 ggctcntgna gcctgctgca cacacagcac atttgcgggc tcctggctct agtgctctgg 660
 ctgggcatct ttggggtgct tggtcctaag caactgccca tacctcactt gactggggga 720
 tgagaaaagg acttagccac ataagatttg ggctcagaaa caaggtcagg tgagtccagg 780
 aagaaaagag aatggttctt gtcttgtaa ccaagtcctt ctcagagtgc caaagacctc 840
 cggattcacc ttggggtag ccagcttacc catcacttac aggttctctc caactctcag 900
 ctgggtctcag tgtcctggat cattagtcac caggctctgt tgagtttcag aaaaataaaa 960
 ggcctctttc cgttcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
 aaactcgagg ggggggcc 1037

<210> 10

<211> 165

<212> PRT

<213> rat

<400> 10

Trp Arg Pro Leu Glx Asn Glx Trp Ile Pro Arg Ala Ala Gly Ile Arg
 1 5 10 15
 His Glu Leu Val Pro Ile Ser Ala Glu Pro Ala Asp Val His Leu Gly
 20 25 30
 Leu Ala Trp Leu Ala Val Gly Ser Met Cys Leu Phe Ile Ala Gly Phe
 35 40 45
 Ala Val Gly Trp Gly Pro Ile Pro Trp Leu Leu Met Ser Glu Ile Phe
 50 55 60
 Pro Leu His Ile Lys Gly Val Ala Thr Gly Val Cys Val Leu Thr Asn
 65 70 75 80
 Trp Phe Met Ala Phe Leu Val Thr Lys Glu Phe Asn Ser Ile Met Glu
 85 90 95
 Ile Leu Arg Pro Tyr Gly Ala Phe Trp Leu Thr Ala Ala Phe Cys Ile
 100 105 110
 Leu Ser Val Leu Phe Thr Leu Thr Phe Val Pro Glu Thr Lys Gly Arg
 115 120 125

Thr Leu Glu Gln Ile Thr Ala His Leu Arg Asp Gly Asp Gly Pro Leu
 130 135 140

Ser Val Thr Gly Ser Pro Glu Leu Ser Trp Leu Arg Val Ser Lys Gly
 145 150 155 160

Val Glu Trp Pro Gln
 165

<210> 11

<211> 282

<212> DNA

<213> mouse

<400> 11

gagcctgctg atgttcacct ggggctggcc tggctggctg taggcagcat gtgcctcttc 60
 atcgctgggtt ttgcagtagg ctgggggaccc atcccctggc tctcatgtc agagatcttc 120
 cctctgcaca tcaaggggtgt ggctaccggc gtctgtgtcc tcaccaactg gttcatggcc 180
 tttctggtga ccaaagagtt taacagcatc atggagatcc tcagacccta cggcgcccttc 240
 tggctcaccg ctgccttctg tctctcagc gtccttttca cg 282

<210> 12

<211> 94

<212> PRT

<213> mouse

<400> 12

Glu Pro Ala Asp Val His Leu Gly Leu Ala Trp Leu Ala Val Gly Ser
 1 5 10 15

Met Cys Leu Phe Ile Ala Gly Phe Ala Val Gly Trp Gly Pro Ile Pro
 20 25 30

Trp Leu Leu Met Ser Glu Ile Phe Pro Leu His Ile Lys Gly Val Ala
 35 40 45

Thr Gly Val Cys Val Leu Thr Asn Trp Phe Met Ala Phe Leu Val Thr
 50 55 60

Lys Glu Phe Asn Ser Ile Met Glu Ile Leu Arg Pro Tyr Gly Ala Phe
 65 70 75 80

Trp Leu Thr Ala Ala Phe Cys Ile Leu Ser Val Leu Phe Thr
 85 90